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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/369,735DATE: 08/26/1999
TIME: 15:33:15

Input Set: I369735.RAW

<p>This Raw Listing contains the General Information Section and up to first 5 pages.</p>

1 <110> APPLICANT: Director-General of Agency of Industrial Science and Technology
 2 <120> TITLE OF INVENTION: Heat-resistant enzyme having - glycosidase activity
 3 <130> FILE REFERENCE: PH-679US
 4 <140> CURRENT APPLICATION NUMBER: US/09/369,735
 5 <141> CURRENT FILING DATE: 1999-08-06
 6 <150> EARLIER APPLICATION NUMBER: JP 10-222866
 7 <160> NUMBER OF SEQ ID NOS: 4
 8 <170> SOFTWARE: PatentIn Ver. 2.0
 9 <210> SEQ ID NO 1
 10 <211> LENGTH: 1269
 11 <212> TYPE: DNA
 12 <213> ORGANISM: Pyrococcus horikoshii
 13 <220> FEATURE:
 14 <221> NAME/KEY: CDS
 15 <222> LOCATION: (1)..(1269)
 16 <400> SEQUENCE: 1

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19	1 5 10 15	
20	tcc cat cag ata gag gga aat aat aga tgg aat gat tgg tgg tac tat	96
21	Ser His Gln Ile Glu Gly Asn Asn Arg Trp Asn Asp Trp Trp Tyr Tyr	
22	20 25 30	
23	gag cag att gga aag ctc ccc tac aga tct ggt aag gct tgc aat cac	144
24	Glu Gln Ile Gly Lys Leu Pro Tyr Arg Ser Gly Lys Ala Cys Asn His	
25	35 40 45	
26	tgg gaa ctt tac agg gat gat att cag cta atg acc agc ttg ggc tat	192
27	Trp Glu Leu Tyr Arg Asp Asp Ile Gln Leu Met Thr Ser Leu Gly Tyr	
28	50 55 60	
29	aat gct tat agg ttc tcc ata gag tgg agc agg cta ttc cca gag gaa	240
30	Asn Ala Tyr Arg Phe Ser Ile Glu Trp Ser Arg Leu Phe Pro Glu Glu	
31	65 70 75 80	
32	aat aaa ttt aat gaa gat gct ttc atg aaa tac cgg gag att ata gac	288
33	Asn Lys Phe Asn Glu Asp Ala Phe Met Lys Tyr Arg Glu Ile Ile Asp	
34	85 90 95	
35	ttg tta ttg acg aga ggt ata act ccc ctg gtg acc cta cac cac ttt	336
36	Leu Leu Leu Thr Arg Gly Ile Thr Pro Leu Val Thr Leu His His Phe	
37	100 105 110	
38	act agc cct ctc tgg ttc atg aag aaa ggt ggc ttc ctt agg gag gag	384
39	Thr Ser Pro Leu Trp Phe Met Lys Lys Gly Gly Phe Leu Arg Glu Glu	
40	115 120 125	
41	aac cta aaa cat tgg gaa aag tac ata gaa aag gtt gct gag ctt tta	432
42	Asn Leu Lys His Trp Glu Lys Tyr Ile Glu Lys Val Ala Glu Leu Leu	
43	130 135 140	
44	gaa aaa gtt aaa cta gta gct acc ttc aat gag ccg atg gta tac gta	480

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45	Glu Lys Val Lys Leu Val Ala Thr Phe Asn Glu Pro Met Val Tyr Val	
46	145 150 155 160	
47	atg atg gga tat cta acg gct tat tgg ccc cca ttc att agg agt cca	528
48	Met Met Gly Tyr Leu Thr Ala Tyr Trp Pro Pro Phe Ile Arg Ser Pro	
49	165 170 175	
50	ttt aag gcc ttt aag gta gct gca aac ctg ctt aaa gct cac gca att	576
51	Phe Lys Ala Phe Lys Val Ala Ala Asn Leu Leu Lys Ala His Ala Ile	
52	180 185 190	
53	gcc tat gaa ctt ctt cat ggg aaa ttc aaa gtt gga atc gta aag aat	624
54	Ala Tyr Glu Leu Leu His Gly Lys Phe Lys Val Gly Ile Val Lys Asn	
55	195 200 205	
56	att ccc ata ata ctc cca gcg agt gac aag gag agg gat aga aaa gcc	672
57	Ile Pro Ile Ile Leu Pro Ala Ser Asp Lys Glu Arg Asp Arg Lys Ala	
58	210 215 220	
59	gct gag aaa gct gat aat tta ttt aac tgg cac ttt ttg gat gcg ata	720
60	Ala Glu Lys Ala Asp Asn Leu Phe Asn Trp His Phe Leu Asp Ala Ile	
61	225 230 235 240	
62	tgg agt ggg aaa tac aga ggg gta ttt aaa aca tat agg att ccc caa	768
63	Trp Ser Gly Lys Tyr Arg Gly Val Phe Lys Thr Tyr Arg Ile Pro Gln	
64	245 250 255	
65	agt gac gca gat ttc att ggg gtt aac tat tac acg gcc agc gaa gta	816
66	Ser Asp Ala Asp Phe Ile Gly Val Asn Tyr Tyr Thr Ala Ser Glu Val	
67	260 265 270	
68	agg cat act tgg aat cct tta aaa ttc ttc ttt gag gtg aaa tta gcg	864
69	Arg His Thr Trp Asn Pro Leu Lys Phe Phe Phe Glu Val Lys Leu Ala	
70	275 280 285	
71	gat att agc gag agg aag act caa atg gga tgg agc gtt tat cca aaa	912
72	Asp Ile Ser Glu Arg Lys Thr Gln Met Gly Trp Ser Val Tyr Pro Lys	
73	290 295 300	
74	gga ata tac atg gcc ctt aaa aaa gct tcc agg tat gga agg cct ctt	960
75	Gly Ile Tyr Met Ala Leu Lys Lys Ala Ser Arg Tyr Gly Arg Pro Leu	
76	305 310 315 320	
77	tat att acg gaa aac gga ata gcg acg ctt gat gat gaa tgg aga gtg	1008
78	Tyr Ile Thr Glu Asn Gly Ile Ala Thr Leu Asp Asp Glu Trp Arg Val	
79	325 330 335	
80	gaa ttc ata att caa cac ctc caa tac gtt cat aag gct atc gaa gac	1056
81	Glu Phe Ile Ile Gln His Leu Gln Tyr Val His Lys Ala Ile Glu Asp	
82	340 345 350	
83	ggc ctg gat gta aga ggt tac ttc tat tgg tca ttt atg gat aac tac	1104
84	Gly Leu Asp Val Arg Gly Tyr Phe Tyr Trp Ser Phe Met Asp Asn Tyr	
85	355 360 365	
86	gag tgg aaa gag ggg ttt ggg cct aga ttt ggc cta gtg gaa gtt gat	1152
87	Glu Trp Lys Glu Gly Phe Gly Pro Arg Phe Gly Leu Val Glu Val Asp	
88	370 375 380	
89	tat caa acc ttc gag aga agg ccc agg aag agt gct tac gta tac gga	1200
90	Tyr Gln Thr Phe Glu Arg Arg Pro Arg Lys Ser Ala Tyr Val Tyr Gly	
91	385 390 395 400	
92	gaa att gca aga agt aag gaa ata aag gat gag cta tta aag aga tat	1248
93	Glu Ile Ala Arg Ser Lys Glu Ile Lys Asp Glu Leu Leu Lys Arg Tyr	
94	405 410 415	

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100     <212> TYPE: PRT
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106     20          25          30
107     Glu Gln Ile Gly Lys Leu Pro Tyr Arg Ser Gly Lys Ala Cys Asn His
108     35          40          45
109     Trp Glu Leu Tyr Arg Asp Asp Ile Gln Leu Met Thr Ser Leu Gly Tyr
110     50          55          60
111     Asn Ala Tyr Arg Phe Ser Ile Glu Trp Ser Arg Leu Phe Pro Glu Glu
112     65          70          75          80
113     Asn Lys Phe Asn Glu Asp Ala Phe Met Lys Tyr Arg Glu Ile Ile Asp
114     85          90          95
115     Leu Leu Leu Thr Arg Gly Ile Thr Pro Leu Val Thr Leu His His Phe
116     100         105         110
117     Thr Ser Pro Leu Trp Phe Met Lys Lys Gly Gly Phe Leu Arg Glu Glu
118     115         120         125
119     Asn Leu Lys His Trp Glu Lys Tyr Ile Glu Lys Val Ala Glu Leu Leu
120     130         135         140
121     Glu Lys Val Lys Leu Val Ala Thr Phe Asn Glu Pro Met Val Tyr Val
122     145         150         155         160
123     Met Met Gly Tyr Leu Thr Ala Tyr Trp Pro Pro Phe Ile Arg Ser Pro
124     165         170         175
125     Phe Lys Ala Phe Lys Val Ala Ala Asn Leu Leu Lys Ala His Ala Ile
126     180         185         190
127     Ala Tyr Glu Leu Leu His Gly Lys Phe Lys Val Gly Ile Val Lys Asn
128     195         200         205
129     Ile Pro Ile Ile Leu Pro Ala Ser Asp Lys Glu Arg Asp Arg Lys Ala
130     210         215         220
131     Ala Glu Lys Ala Asp Asn Leu Phe Asn Trp His Phe Leu Asp Ala Ile
132     225         230         235         240
133     Trp Ser Gly Lys Tyr Arg Gly Val Phe Lys Thr Tyr Arg Ile Pro Gln
134     245         250         255
135     Ser Asp Ala Asp Phe Ile Gly Val Asn Tyr Tyr Thr Ala Ser Glu Val
136     260         265         270
137     Arg His Thr Trp Asn Pro Leu Lys Phe Phe Phe Glu Val Lys Leu Ala
138     275         280         285
139     Asp Ile Ser Glu Arg Lys Thr Gln Met Gly Trp Ser Val Tyr Pro Lys
140     290         295         300
141     Gly Ile Tyr Met Ala Leu Lys Lys Ala Ser Arg Tyr Gly Arg Pro Leu
142     305         310         315         320
143     Tyr Ile Thr Glu Asn Gly Ile Ala Thr Leu Asp Asp Glu Trp Arg Val
144     325         330         335

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145      Glu Phe Ile Ile Gln His Leu Gln Tyr Val His Lys Ala Ile Glu Asp
146                340                345                350
147      Gly Leu Asp Val Arg Gly Tyr Phe Tyr Trp Ser Phe Met Asp Asn Tyr
148                355                360                365
149      Glu Trp Lys Glu Gly Phe Gly Pro Arg Phe Gly Leu Val Glu Val Asp
150                370                375                380
151      Tyr Gln Thr Phe Glu Arg Arg Pro Arg Lys Ser Ala Tyr Val Tyr Gly
152      385                390                395                400
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154                405                410                415
155      Gly Leu Pro Glu Leu Gln Leu
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157 <210> SEQ ID NO 3
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159 <212> TYPE: DNA
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162 <223> OTHER INFORMATION: Description of Artificial Sequence:An upper primer designe
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164 <400> SEQUENCE: 3
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168 <212> TYPE: DNA
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170 <220> FEATURE:
171 <223> OTHER INFORMATION: Description of Artificial Sequence:A lower primer designed
172      create the BamHI site.
173 <400> SEQUENCE: 4
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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text
